

	Type	L #	Hits	Search Text	DBs
1	BRS	L1	3	MOSCOW-JEFFREY-A	US-PGPUB; USPAT; EPO; JPO; DERWENT
2	BRS	L2	27	LU-XIN	US-PGPUB; USPAT; EPO; JPO; DERWENT
3	BRS	L4	31	JORDAN-C	US-PGPUB; USPAT; EPO; JPO; DERWENT
4	BRS	L5	4	JORDAN-CRAIG	US-PGPUB; USPAT; EPO; JPO; DERWENT
5	BRS	L7	8	OKB1	US-PGPUB; USPAT; EPO; JPO; DERWENT
6	BRS	L8	143	organic adj cation adj transporter	US-PGPUB; USPAT; EPO; JPO; DERWENT
7	BRS	L9	71	OCT-6	US-PGPUB; USPAT; EPO; JPO; DERWENT
8	BRS	L11	30	OCT-6 and leukemia	US-PGPUB; USPAT; EPO; JPO; DERWENT
9	BRS	L12	3	OCT-6 same leukemia	US-PGPUB; USPAT; EPO; JPO; DERWENT
10	BRS	L13	0	OCT-6 with leukemia	US-PGPUB; USPAT; EPO; JPO; DERWENT
11	BRS	L14	56	OCT6	US-PGPUB; USPAT; EPO; JPO; DERWENT
12	BRS	L15	0	OCT6 with leukemia	US-PGPUB; USPAT; EPO; JPO; DERWENT
13	BRS	L16	0	OCT6 with cancer	US-PGPUB; USPAT; EPO; JPO; DERWENT
14	BRS	L10	35	OCT-6 and cancer	US-PGPUB; USPAT; EPO; JPO; DERWENT
15	BRS	L17	15	OCT6 and malignan\$	US-PGPUB; USPAT; EPO; JPO; DERWENT
16	BRS	L18	0	OCT6 same malignan\$	US-PGPUB; USPAT; EPO; JPO; DERWENT
17	BRS	L19	1	OCT-6 same malignan\$	US-PGPUB; USPAT; EPO; JPO; DERWENT

BBB  
10/849,551

Set	Items	Description
S1	12	AU='MOSCOW, JA'
S2	2	AU='MOSCOW, JEFFREY A'
S3	8	AU='MOSCOW J'
S4	105	AU='MOSCOW J A'
S5	67	AU='MOSCOW J.A.'
S6	49	AU='MOSCOW JA'
S7	51	AU='MOSCOW JEFFREY A'
S8	56	AU='JORDAN, C'
S9	494	AU='JORDAN, C.'
S10	1	AU='JORDAN, CRAIG ALAN'
S11	10	AU='JORDAN, CRAIG T'
S12	951	AU='JORDAN C'
S13	51	AU='JORDAN C A'
S14	62	AU='JORDAN C T'
S15	16	AU='JORDAN C.A.'
S16	69	AU='JORDAN C.T.'
S17	11	AU='JORDAN CRAIG'
S18	68	AU='JORDAN CRAIG T'
S19	241	AU='LU, X'
S20	94	AU='LU, XIN'
S21	4	AU='LU, XIN*'
S22	298	AU='LU XIN'
S23	52	TRANSPORTER AND (S1 OR S2 OR S3 OR S4 OR S5 OR S6 OR S7 OR S8 OR S9 OR S10 OR S11 OR S12 OR S13 OR S14 OR S15 OR S16 OR - S17 OR S18 OR S19 OR S20 OR S21 OR S22)
S24	18	RD (unique items)
S25	173	OCT6
S26	54	RD (unique items)
S27	83	OCT-6
S28	66	RD (unique items)
S29	2	S28 AND LEUKEMIA
S30	15	OKB1
S31	10	RD (unique items)
S32	2297	ORGANIC(W) CATION(W) TRANSPORTER
S33	48	S32 AND HEMAT?
S34	23	RD (unique items)
S35	65	SLC22
S36	25	RD (unique items)
S37	33	S32 AND LEUKEMIA
S38	16	RD (unique items)
S39	0	S32 AND MALIGAN?
S40	19	S32 AND MALIGNAN?
S41	12	RD (unique items)
S42	96	S32 AND CANCER
S43		

10/849,551  
 DIALOG  
 file biosci  
 6/2/06  
 BOB

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OM protein - protein search, using sw model

Run on: April 24, 2006, 21:59:16 ; Search time 190 Seconds  
(without alignments)  
1336.637 Million cell updates/sec

Title: US-10-849-551-2  
Perfect score: 3005  
Sequence: 1 MGSRHFEGIYDHVGHFGRFQ.....NNSGLEKTEAITPRDSGLGE 578

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2989.5	99.5	577	7 ADC77507	Adc77507 Human org
2	2989.5	99.5	577	9 ADZ88883	Adz88883 Human put
3	2988.5	99.5	577	4 AAM78367	Aam78367 Human pro
4	2988.5	99.5	577	5 ABP74100	Abp74100 Human TRI
5	2967	98.7	584	4 AAM00930	Aam00930 Human bon
6	2933.5	97.6	585	4 AAM79351	Aam79351 Human pro
7	2888.5	96.1	560	3 AAB43038	Aab43038 Human ORF
8	2748.5	91.5	534	5 ABP53582	Abp53582 Human NOV
9	2748.5	91.5	534	8 ADH42227	Adh42227 Novel hum
10	2695.5	89.7	543	6 ABP58994	Abp58994 Human tes
11	2651.5	88.2	515	8 ADH42225	Adh42225 Novel hum
12	2515.5	83.7	526	5 ABP53583	Abp53583 Human NOV
13	2515.5	83.7	526	8 ADH42229	Adh42229 Novel hum
14	2297.5	76.5	509	8 ADH42223	Adh42223 Novel hum
15	2282.5	76.0	483	4 AAM00982	Aam00982 Human bon
16	1791.5	59.6	361	6 ADA55481	Ada55481 Human pro
17	1721.5	57.3	342	5 AAE22916	Aae22916 Human tra
18	1100	36.6	302	4 AAM00817	Aam00817 Human bon
19	829.5	27.6	567	4 ABB68354	Abb68354 Drosophil
20	799	26.6	548	4 ABB62279	Abb62279 Drosophil
21	782	26.0	557	2 AAY01650	Aay01650 A protein
22	782	26.0	557	3 AAY83929	Aay83929 Human car
23	782	26.0	557	4 ABG03029	Abg03029 Novel hum
24	782	26.0	557	6 ABB82979	Abb82979 Human SLC
25	782	26.0	557	6 ABB82980	Abb82980 Human SLC
26	782	26.0	557	6 ABO07242	Abo07242 Human p53
27	782	26.0	557	7 ADE09321	Ade09321 Novel pro
28	782	26.0	557	7 ADE09261	Ade09261 Novel pro
29	782	26.0	557	8 ADP23817	Adp23817 PRO polyp
30	782	26.0	557	9 ADY79867	Ady79867 Amino aci
31	781	26.0	551	6 ABR62439	Abr62439 Human cat
32	780	26.0	551	6 ABB82977	Abb82977 Human SLC
33	777	25.9	551	2 AAY01649	Aay01649 A protein

34	777	25.9	551	6	ABB82978	Abb82978 Human SLC
35	777	25.9	551	6	ABR62440	Abr62440 Human cat
36	777	25.9	551	9	ADY84982	Ady84982 Human org
37	756	25.2	191	4	AAU87130	Aau87130 Novel cen
38	756	25.2	191	4	ADM19908	Adm19908 Protein e
39	756	25.2	191	8	ADI54445	Adi54445 Novel hum
40	738	24.6	553	2	AAY01651	Aay01651 A protein
41	738	24.6	553	3	AAB20579	Aab20579 Mouse OCT
42	735.5	24.5	564	3	AAB20578	Aab20578 Mouse OCT
43	718	23.9	557	2	AAY01652	Aay01652 A protein
44	718	23.9	557	3	AAB20580	Aab20580 Mouse OCT
45	718	23.9	557	3	AAY83930	Aay83930 Mouse car

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OM protein - protein search, using sw model

Run on: April 24, 2006, 22:07:02 ; Search time 46 Seconds  
 (without alignments)  
 1038.838 Million cell updates/sec

Title: US-10-849-551-2  
 Perfect score: 3005  
 Sequence: 1 MGSRRHFEGIYDHVGHFGRFQ.....NNSGLEKTEAITPRDSGLGE 578

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	782	26.0	557	2	US-10-327-189-4
2	782	26.0	557	2	US-09-521-195B-3
3	782	26.0	557	2	US-09-798-743-1
4	782	26.0	557	2	US-09-949-016-6309
5	781	26.0	551	2	US-10-327-189-38
6	780	26.0	551	2	US-10-327-189-2
7	777	25.9	551	2	US-10-327-189-7
8	777	25.9	551	2	US-09-521-195B-1
9	738	24.6	553	2	US-09-521-195B-22
10	738	24.6	610	2	US-09-949-016-7929
11	718	23.9	557	2	US-09-521-195B-27
12	718	23.9	557	2	US-09-798-743-3
13	666	22.2	538	2	US-09-614-891-9
14	664.5	22.1	546	2	US-09-614-891-8
15	656	21.8	547	2	US-09-949-016-7043
16	650.5	21.6	553	2	US-08-501-572-2
17	650.5	21.6	553	2	US-09-040-444-2
18	641	21.3	555	2	US-08-501-572-3
19	641	21.3	555	2	US-09-040-444-3
20	631	21.0	556	2	US-08-501-572-1
21	631	21.0	556	2	US-09-040-444-1
22	622	20.7	556	2	US-09-949-016-7027
23	622	20.7	565	2	US-09-949-016-10036
24	611.5	20.3	554	2	US-09-949-016-10978
25	601.5	20.0	542	2	US-09-614-891-10
26	599.5	20.0	545	2	US-09-572-147-2
27	597.5	19.9	550	2	US-09-330-245A-2
28	597.5	19.9	550	2	US-09-614-891-7
29	581.5	19.4	537	1	US-08-647-397-2
30	456	15.2	609	2	US-09-949-016-10979
31	452	15.0	541	2	US-09-614-891-12
32	448.5	14.9	550	2	US-09-786-261-2
33	428	14.2	554	2	US-09-614-891-11
34	317	10.5	439	2	US-09-602-787A-514
35	292.5	9.7	456	2	US-09-328-352-5446
36	280.5	9.3	475	2	US-09-328-352-5706

37	274	9.1	519	2	US-09-720-655B-1	Sequence 1, Appli
38	274	9.1	520	2	US-08-964-127-2	Sequence 2, Appli
39	274	9.1	520	2	US-09-496-692-2	Sequence 2, Appli
40	274	9.1	520	2	US-10-000-273-2	Sequence 2, Appli
41	273.5	9.1	218	2	US-09-270-767-33194	Sequence 33194, A
42	273.5	9.1	218	2	US-09-270-767-48411	Sequence 48411, A
43	265.5	8.8	446	2	US-09-543-681A-6579	Sequence 6579, Ap
44	259.5	8.6	447	2	US-09-252-991A-20563	Sequence 20563, A
45	246.5	8.2	506	2	US-09-252-991A-17560	Sequence 17560, A

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OM protein - protein search, using sw model

Run on: April 24, 2006, 22:09:37 ; Search time 166 Seconds  
 (without alignments)  
 1454.852 Million cell updates/sec

Title: US-10-849-551-2  
 Perfect score: 3005  
 Sequence: 1 MGSRRHFEGIYDHVGHFGRFQ.....NNSGLEKTEAITPRDSGLGE 578

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*  
 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2989.5	99.5	577	4	US-10-038-854-163
2	2748.5	91.5	534	4	US-10-038-854-28
3	2695.5	89.7	543	5	US-10-479-013A-2
4	2515.5	83.7	526	4	US-10-038-854-30
5	2378.5	79.2	456	4	US-10-038-854-164
6	2145.5	71.4	419	4	US-10-038-854-371
7	1791.5	59.6	361	4	US-10-094-749-3049
8	1791.5	59.6	361	4	US-10-038-854-165
9	1721.5	57.3	342	4	US-10-380-727-15
10	1550	51.6	305	4	US-10-038-854-166
11	1002.5	33.4	198	4	US-10-038-854-369
12	848	28.2	419	4	US-10-038-854-167
13	829.5	27.6	567	6	US-11-097-143-31854
14	799	26.6	548	6	US-11-097-143-13629
15	782	26.0	557	3	US-09-798-743A-1
16	782	26.0	557	4	US-10-762-154-3
17	782	26.0	557	4	US-10-327-188-4
18	782	26.0	557	5	US-10-940-500-1
19	782	26.0	557	5	US-10-450-763-33388
20	781	26.0	551	4	US-10-327-188-38
21	780	26.0	551	4	US-10-327-188-2
22	777	25.9	551	4	US-10-762-154-1
23	777	25.9	551	4	US-10-327-188-7
24	756	25.2	191	3	US-09-764-875-648
25	738	24.6	553	4	US-10-762-154-22
26	735.5	24.5	564	5	US-10-968-848-83
27	718	23.9	557	3	US-09-798-743A-3
28	718	23.9	557	4	US-10-762-154-27
29	718	23.9	557	5	US-10-940-500-3
30	718	23.9	557	5	US-10-968-848-82
31	687.5	22.9	557	6	US-11-097-143-41202
32	683.5	22.7	553	5	US-10-968-848-76
33	666	22.2	538	5	US-10-721-298-9
34	664.5	22.1	540	5	US-10-968-848-85
35	664.5	22.1	546	5	US-10-721-298-8
36	661	22.0	539	4	US-10-408-765A-1292

37	657.5	21.9	552	4	US-10-276-774-2400	Sequence 2400, Ap
38	657	21.9	556	5	US-10-968-848-75	Sequence 75, Appl
39	645	21.5	554	5	US-10-643-795A-82	Sequence 82, Appl
40	645	21.5	554	5	US-10-948-518-82	Sequence 82, Appl
41	645	21.5	555	5	US-10-936-626-105	Sequence 105, App
42	645	21.5	555	5	US-10-938-061-105	Sequence 105, App
43	644	21.4	555	4	US-10-295-027-300	Sequence 300, App
44	644	21.4	555	4	US-10-712-124-118	Sequence 118, App
45	644	21.4	555	5	US-10-936-626-104	Sequence 104, App



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OM protein - protein search, using sw model

Run on: April 24, 2006, 22:10:27 ; Search time 27 Seconds  
 (without alignments)  
 941.988 Million cell updates/sec

Title: US-10-849-551-2  
 Perfect score: 3005  
 Sequence: 1 MGSRRHFEGYIDHVGHFGRFQ.....NNSGLEKTEAITPRDSGLGE 578

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications\_AA\_New:\*  
 1: /SIDS5/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
 2: /SIDS5/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
 3: /SIDS5/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
 4: /SIDS5/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
 5: /SIDS5/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
 6: /SIDS5/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
 7: /SIDS5/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
 8: /SIDS5/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	657	21.9	535	6	US-10-507-755-5
2	608.5	20.2	542	6	US-10-507-755-6
3	607.5	20.2	551	6	US-10-055-877-276
4	607.5	20.2	551	6	US-10-055-877-277
5	597.5	19.9	550	6	US-10-055-877-274
6	597.5	19.9	550	6	US-10-055-877-275
7	594	19.8	563	6	US-10-055-877-273
8	594	19.8	563	7	US-11-259-417-2
9	594	19.8	563	7	US-11-259-417-4
10	573	19.1	553	6	US-10-203-486-9
11	568.5	18.9	556	6	US-10-055-877-81
12	565	18.8	643	6	US-10-507-755-4
13	542.5	18.1	573	6	US-10-055-877-79
14	496	16.5	705	7	US-11-124-367A-353
15	458.5	15.3	553	6	US-10-507-755-1
16	448.5	14.9	550	7	US-11-043-889-5
17	446.5	14.9	566	6	US-10-203-486-13
18	434.5	14.5	550	6	US-10-507-755-7
19	361	12.0	347	6	US-10-055-877-269
20	361	12.0	347	6	US-10-055-877-270
21	361	12.0	347	6	US-10-055-877-271
22	342	11.4	332	6	US-10-511-538-79
23	340	11.3	359	6	US-10-055-877-272
24	338	11.2	500	7	US-11-188-298-14951
25	318	10.6	588	7	US-11-188-298-14702
26	316.5	10.5	572	7	US-11-043-889-13
27	312	10.4	451	7	US-11-188-298-21140
28	311	10.3	487	6	US-10-055-877-268
29	288.5	9.6	452	7	US-11-188-298-5405
30	284.5	9.5	589	7	US-11-188-298-11139
31	277	9.2	449	7	US-11-188-298-3550
32	277	9.2	449	7	US-11-188-298-9203
33	262.5	8.7	464	7	US-11-188-298-1901
34	259.5	8.6	443	7	US-11-188-298-4870

35	259.5	8.6	472	7	US-11-188-298-1544	Sequence 1544, Ap
36	258.5	8.6	443	7	US-11-188-298-1772	Sequence 1772, Ap
37	258.5	8.6	443	7	US-11-188-298-6936	Sequence 6936, Ap
38	252	8.4	491	7	US-11-188-298-8641	Sequence 8641, Ap
39	249.5	8.3	446	7	US-11-188-298-19232	Sequence 19232, A
40	249	8.3	491	7	US-11-188-298-645	Sequence 645, App
41	247.5	8.2	446	7	US-11-188-298-11070	Sequence 11070, A
42	243	8.1	461	7	US-11-096-568A-28485	Sequence 28485, A
43	239	8.0	461	7	US-11-188-298-20775	Sequence 20775, A
44	234	7.8	579	7	US-11-188-298-20145	Sequence 20145, A
45	232.5	7.7	442	7	US-11-188-298-7549	Sequence 7549, Ap

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OM protein - protein search, using sw model

Run on: April 24, 2006, 21:59:40 ; Search time 232 Seconds  
 (without alignments)  
 1757.739 Million cell updates/sec

Title: US-10-849-551-2  
 Perfect score: 3005  
 Sequence: 1 MGSRRHFEGIYDHVGHFGRFQ.....NNSGLEKTEAITPRDSGLGE 578

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : UniProt\_05.80:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2989.5	99.5	577	2	Q96RU0_HUMAN	Q96ru0 homo sapien
2	2988.5	99.5	577	2	Q86VW1_HUMAN	Q86vw1 homo sapien
3	2982.5	99.3	577	2	Q8IZD5_HUMAN	Q8izd5 homo sapien
4	2695.5	89.7	543	2	Q8IUG8_HUMAN	Q8iug8 homo sapien
5	2378.5	79.2	456	2	O14567_HUMAN	O14567 homo sapien
6	2187.5	72.8	432	2	Q5JXM1_HUMAN	Q5jxm1 homo sapien
7	1791.5	59.6	361	2	Q96M90_HUMAN	Q96m90 homo sapien
8	1763	58.7	575	2	Q66KG0_XENLA	Q66kg0 xenopus lae
9	1387.5	46.2	565	2	Q5TZ30_BRARE	Q5tz30 brachydanio
10	1364	45.4	563	2	Q4S705_TETNG	Q4s705 tetraodon n
11	978	32.5	177	2	Q96ER0_HUMAN	Q96er0 homo sapien
12	829.5	27.6	567	1	OCTL_DROME	Q95r48 drosophila
13	807.5	26.9	525	2	Q7QAC5_ANOGA	Q7qac5 anopheles g
14	799	26.6	548	1	ORCT_DROME	Q9vca2 drosophila
15	790.5	26.3	557	2	Q5W4T3_CHICK	Q5w4t3 gallus gall
16	782	26.0	557	1	OCTN2_HUMAN	O76082 homo sapien
17	781	26.0	551	1	OCTN1_HUMAN	Q9h015 homo sapien
18	759	25.3	548	2	Q7TOW2_XENLA	Q7t0w2 xenopus lae
19	738	24.6	553	1	OCTN1_MOUSE	Q9z306 mus musculu
20	738	24.6	553	2	Q5SWV1_MOUSE	Q5swv1 mus musculu
21	735.5	24.5	564	1	OCTN3_MOUSE	Q9wtn6 mus musculu
22	735.5	24.5	564	2	Q5SWV0_MOUSE	Q5swv0 mus musculu
23	731	24.3	553	1	OCTN1_RAT	Q9r141 rattus norv
24	725.5	24.1	553	2	Q6P3Q3_XENTR	Q6p3q3 xenopus tro
25	724	24.1	557	1	OCTN2_RAT	O70594 rattus norv
26	718	23.9	557	1	OCTN2_MOUSE	Q9z0e8 mus musculu
27	718	23.9	557	2	Q5SX17_MOUSE	Q5sx17 mus musculu
28	700	23.3	554	2	O77504_RABIT	O77504 oryctolagus
29	699.5	23.3	553	2	Q6P695_BRARE	Q6p695 brachydanio
30	697.5	23.2	555	2	Q961R9_DROME	Q961r9 drosophila
31	683.5	22.7	553	2	O70577_MOUSE	O70577 mus musculu
32	683	22.7	566	2	Q63ZS1_XENLA	Q63zs1 xenopus lae
33	674.5	22.4	544	2	Q8BWF6_MOUSE	Q8bwf6 mus musculu
34	668	22.2	535	2	Q5RLM2_RAT	Q5rlm2 rattus norv
35	664.5	22.1	540	2	Q8K4S9_MOUSE	Q8k4s9 mus musculu
36	664.5	22.1	540	2	Q91WU2_MOUSE	Q91wu2 mus musculu
37	663.5	22.1	546	2	Q5T048_HUMAN	Q5t048 homo sapien
38	663	22.1	539	2	Q5T050_HUMAN	Q5t050 homo sapien
39	662	22.0	562	2	Q7T2C0_BRARE	Q7t2c0 brachydanio
40	661	22.0	539	2	Q9H2W5_HUMAN	Q9h2w5 homo sapien

41	659.5	21.9	548	2	Q5R540_PONPY	Q5r540	pongo	pygma
42	659	21.9	535	2	Q63314_RAT	Q63314	rattus	norv
43	657	21.9	556	2	Q9R1Q4_MOUSE	Q9r1q4	mus	musculu
44	655.5	21.8	548	2	Q9Y694_HUMAN	Q9y694	homo	sapien
45	654	21.8	556	2	O08966_MOUSE	O08966	mus	musculu

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: April 24, 2006, 22:03:06 ; Search time 43 Seconds  
 (without alignments)  
 1293.332 Million cell updates/sec

Title: US-10-849-551-2  
 Perfect score: 3005  
 Sequence: 1 MGSRRHFEGIIYDHVGHFGRFQ.....NNSGLEKTEAITPRDGLGE 578

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR 80:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	782	26.0	557	2	JW0089	organic cation tra
2	715	23.8	557	2	JE0346	high-affinity carn
3	644.5	21.4	576	2	T22509	hypothetical prote
4	634.5	21.1	593	2	JC4884	organic cation tra
5	631	21.0	556	2	S50862	organic cation tra
6	525.5	17.5	745	2	T16565	hypothetical prote
7	493.5	16.4	794	2	T27870	hypothetical prote
8	434	14.4	447	2	D89646	protein ZK455.8 [i
9	421	14.0	751	2	C88485	protein F23F12.5 [
10	406	13.5	448	2	AC3602	transporter, mfs s
11	391	13.0	450	2	F95360	probable transmemb
12	390	13.0	539	2	C96758	probable protein
13	376	12.5	437	2	G97630	probable sugar tra
14	376	12.5	437	2	AB2854	MFS permease [impo
15	361.5	12.0	454	2	F75580	probable sugar tra
16	354.5	11.8	540	2	T25851	hypothetical prote
17	347.5	11.6	528	2	T21682	hypothetical prote
18	331.5	11.0	518	2	B86299	hypothetical prote
19	310.5	10.3	461	2	AE3208	MFS permease [impo
20	304	10.1	480	2	T23608	hypothetical prote
21	302.5	10.1	527	2	T01019	transport protein
22	302.5	10.1	1222	2	C88504	protein B0361.3 [i
23	288.5	9.6	521	2	H86298	hypothetical prote
24	285	9.5	517	2	T19962	hypothetical prote
25	283	9.4	515	2	B96825	hypothetical prote
26	282	9.4	541	2	T28069	hypothetical prote
27	279	9.3	422	2	G72234	hypothetical prote
28	277	9.2	510	2	B88381	protein T22F7.1 [i
29	275.5	9.2	478	2	T33985	hypothetical prote
30	269	9.0	529	2	T23190	hypothetical prote
31	259.5	8.6	443	2	H85485	probable transport
32	259.5	8.6	443	2	H90634	probable transport
33	259	8.6	520	2	T23545	hypothetical prote
34	258.5	8.6	443	2	E64725	yaaU protein - Esc
35	257	8.6	532	2	T27235	hypothetical prote
36	256	8.5	517	2	T20174	hypothetical prote
37	255.5	8.5	442	2	A83122	probable MFS trans
38	252.5	8.4	455	2	B83213	probable MFS trans

39	246.5	8.2	524	2	T27082	hypothetical prote
40	245	8.2	461	2	D70073	metabolite transpo
41	243	8.1	461	2	G85059	probable sugar tra
42	241	8.0	742	2	S27263	synaptic vesicle p
43	239	8.0	742	1	A43344	synaptic vesicle p
44	237.5	7.9	404	2	T19922	hypothetical prote
45	235.5	7.8	423	2	S74046	probable sugar tra